Nuclectide sequenc Xylanase xynD gene Thermostable alkal Actinomadura sp. D Actinomadura flexu

AAX90405 AAX15063 AAV15063 AAV36098 AAT42374

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AAT08142

pumilus xylanas

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	Description	Xylanase gene. Ba	Xylanase precursor	Xylanase gene. Ba	Glycosyl hydrolase	DNA encoding a Bac	Thermostable alkal	Xylanase activity	Clostridium sterco
SUMMARIES	ΙD	AAT16101	AAT16102	AAT16103	AAV13067	AAV30255	AAQ92878	AAV13074	AAZ51821
	DB	17	11	11	19	19	16	19	21
	% Query Match Length DB ID	100.0 663	744	1513	744	871	744	747	2364
	% Query Match	100.0	100.0	100.0	95.7	95.7	94.2	9.92	38.5
	Score	699	663	663	634.2	634.2	624.6	507.8	255.4
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υ	16	119	17	σ.	229	13	AAV15063		Xylanase activity	
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	1 6	115.2	11	. 4.	213	13	AAV15059		XVlanase activity	
	20	115.2	17	4.	596	21	AAA48219		T. reesei xylanase	
	21	115.2	17	4.0	596	24	AAD29410		Trichoderma reesei	
	2 6	108.2	19	ייי יי	801	22	AA166600		Ayianase Ayna gene Bacillus haloduran	
	24	106	16	. 0.	2898	21	AAZ46404		Penicillium funicu	
	25	105.8	16	0.	1195	20	AAZ28864		Streptomyces oliva	
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	29	100.8	12	. ~	1581	12	AAQ69150		Aspergillus tubige	
	30	100.8	15	~	3105	21	AAZ51819		Ruminococcus xylan	
	31	100.4	15	٦.	234	13	AAV15064		Xylanase activity	
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	12 r	96	14		1027	225	AAF85591		Acremonium cellulo	
	36	93.4	14	·	675	14	AAQ36563		Endo-xylanase gene	
	37	92	13	6.	164	16	AAQ92877		Thermostable alkal	
	38	91	13	۲.	1015	14	AAQ54775		T. reesei xln2 gen	
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S	Bac	Bacillus s	sp. s	strain	710/1	1 (LMG	MG P-14798).			
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Best Local Similarity 100
Matches 663; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (AAR92053) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). Sequences were also obtd. Gee AAT16102 and AAT16103) for the xylanase precursor and for the complete gene including 5' and 3' untranslated sequences. DNA coding for the mature enzyme may be incorporated into a vector and expressed from either its own promoter or from the Bacillus pumilus PLL B12 promoter (AAQ73996) and used for prodn. of recombinant xylanase in transformed hosts, pref. Bacillus licheniformis or B. pumilus. The enzyme is useful in the paper-pulp, animal feed and baking industries.
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DB; AAR92053.
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AAT 663
                                                  ATTAACGGTAACCCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC
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                              ATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC
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Matches 663
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P-PSDB; AAR92054.
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26-JUL-1994;
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94BE-0000706
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82..744
/*tag= b
/EC_number=
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                                                                                                                                                                                                                                                     Score 663; DB 17;
Pred. No. 1.4e-188;
D; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                        T; 0 other;
                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          goods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used
                                                                                                                                                                                                                                                                                                            744;
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A DNA sequence (AAT16102) coding for a xylanase precursor (AAR92054) was isolated from a gene library of Bacillus sp. 720/1 (LMG P-14798). The gene may be incorporated into a vector and expressed in transformed hosts, pref. Bacillus licheniformis or Bacillus pumilus, for prodn. of thermostable mature xylanase (AAR92053). The enzyme is useful in the paper pulp, animal feed and baking industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                 701 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTTATGCGCTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1061 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1121 TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001 TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGGACCATCACTGTTGATGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                   CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAAATTTTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>AACCACTTTAGAGCGTGGGAAAACTTAGGGGATGAATATGGGGAAAATGTATGAAGTCGCG</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 663; DB 17; Length 1513;
Best Local Similarity 100.0%; Pred. No. 1.9e-188;
Matches 663; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                 ij
                                                                                                                                                                  goods
                                                                                                                                                                                                                                                                                                                                Sequence 1513 BP; 500 A; 282 C; 271 G; 460 T; 0 other;
                                                                                                                                                               Bacillus derived xylanase active over wide pH range treatment of paper pulp, animal feeds and in bakery
                                                                                                ä
                                                                                                Ledoux
                                                                                                                                                                                                         Claim 10; Page 59-61; 94pp; English
                                                                                                Lahaye A,
                 95BE-0000448.
94BE-0000706.
                                                                                                Detroz R,
                                                       (SOLV ) SOLVAY SA.
(SOLV ) SOLVAY & CIE.
                                                                                                                         WPI; 1996-117341/13.
P-PSDB; AAR92054.
                 17-MAY-1995;
26-JUL-1994;
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                                          TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
                                                                                                                                                    TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
                                                                                                                                                                   TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
                                                                                                                                                                                                         ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA
                                                                                                                                                                                                                                                               TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGGCACGATTTCTGTCAGC
                                                                                                                                                                                                                                                                                                                   AACCACTITAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCG
                                                                                                                                                                                                                                                                                                                                                                        CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermostable enzyme; paper; pulp; bleaching; feedstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain 710/1 (LMG P-14798)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
620.1366
/*tag= b
620.600
/*tag= c
701.1363
/*tag= c
/EC number= 3.2.1.8
1367.1513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xylanase, the baking, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU9525086-A.
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RESULT 3 AAT16103

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                                                                                                           Matches
                                                                                                                      Query Match
Best Local
                                                                                                                                                               Sequence 744 BP;
                                                                                                                                                                                                  The present sequence encodes a polypeptide with xylanase activity used in an example of the present invention. The present invention describes a novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interest. The method comprises:

(i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence and a 3' structural gene sequence; (iii) expressing the resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequence encoding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms
                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 31-32; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microorganism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosyl
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                                                                                                                                                                                                                                                                                                                                                                                                         Isolating novel DNA sequences from for culturing the microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dalboge H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1996;
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142
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                                                                                                                        Similarity
GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
                GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
                                                     CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
                                                                      CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTTGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diderichsen B,
                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                          to cultivate and isolate the microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96DK-0000562
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1..747
                                                                                                                                                              249 A; 146 C; 157 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "glycosyl hydrolase family 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     '*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family 11 xylanase DNA derived from Bacillus
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                                                                                                                     95.7%;
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                                                                                                                      Score 634.2;
Pred. No. 6e
                                                                                                            Mismatches
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                                                                                                                        6e-180;
                                                                                                                                   DB 19;
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                                                                                                            Indels
                                                                                                                                   Length 744;
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02-JUL-1993;
30-NOV-1994;
06-JUN-1995;
                                                                                                                                                                                                     Xylanolytic enzyme; Bacillus agaradherens NCIMB 40482; breakdown; agricultural waste; alcohol fuel; enzymatic treatment; animal feed; release; free pentose sugar; dissolving pulp; cellulose; bio-bleaching; wood pulp; lignocellulostic material; animal feed additive; ss.
                                                                                                                                          CDS
                                                                                                                                                                             Bacilluc agaradherens.
                                                                                                                                                                                                                                                                    DNA encoding a Bacillus agaradherens xylanolytic enzyme
                                                                                                                                                                                                                                                                                             25-MAR-2003
18-AUG-1998
                                                                                                                                                                                                                                                                                                                                    AAV30255;
                                                                                                                                                                                                                                                                                                                                                            AAV30255
                                                   16-AUG-1996;
                                                                           23-JUN-1998
                                                                                                     US5770424-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                661
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                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTAACGGTAACCCTCTCAACTATTAGTAATGACAAGAGCATAACTCTAGATAAAAAC
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(first entry)
93WO-DK00218.
94US-0343600.
95US-0470398.
                                                  96US-0698978
                                                                                                                                          Location/Qualifiers 82..747
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CAAATCGTCACCGACAATTCCATTGCCACCCGCGGTGGTTATGATTATGAATTTTGGAAA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from Bacillus sp. 1-43-3. Fragments of the sequence (e.g. the internal fragments given in AAQ92876 and AAQ92877) may be amplified by polymerase chain reaction, e.g. using primers with sequences AAQ92866, AAQ92866, AAQ92868 and AAQ92869. The DNA may be cloned in Escherichia coli using a plasmid vector for recombinant xylanase production. The xylanase may be used in the paper and pulp industries, where it produces an increase in $ 180 brightness softwood pulp of at least 1.0 over non-enzymatically treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg C. The enzyme may be used in production of paper, board and fluff pulp, and has low cellulase activity. The increased brightness produced using the xylanase allows reduction in the amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encodes an alkaline endo-1,4-beta-D-xylanase (G-type)
                                                                                                                                                                                                                                                                                                                                  thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning; polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper; pulp; bleaching; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.2%; Score 624.6; DB 16; Length 744; 96.4%; Pred. No. 4.6e-177; ive 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful in paper and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 744 BP; 248 A; 145 C; 159 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                               Thermostable alkaline endo-1,4-beta-D-xylanase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbes WT, Herweijer M
, Van Beckhoven RFWC;
en P, Williams DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel xylanase enzyme active at high pH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ME, Quax WJ, Van
Van Solingen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 42-43; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus sp. 1-43-3 (CBS 672.93)
                                                                                                                                                                                    AAQ92878 standard; DNA; 744 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93EP-0203694.
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Matches 639; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Farrell RL, Goedegebuur F, Iverson S, Jones BE, Quax
                                                                                                                                                                                                                                                            12-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KONN ) GIST-BROCADES NV.
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Van der Kleij WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR76551
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                                                      AAT 663
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                                                      661
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                                                                                                                                             RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                      Jorgensen PL;
                                                                                                                                                                                                                                                                                         The present sequence encodes a xylanolytic enzyme of Bacillus agaradherens NCIMB 40482. Xylanolytic enzymes are used for enzymatic breakdown of sgricultural wastes for production of alcohol fuels, enzymatic treatment of animal feeds to release free pentose sugars, manufacturing of dissolving pulps yielding cellulose and bio-bleaching of wood pulp. They are also used for treatment of lignocellulostic material e.g. paper and pulp, or as an animal feed additive. (Updated on 25-WAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
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                                                                                                                                                             DNA construct encoding Bacillus agaradherens xylanolytic enzyme - and vectors and Bacillus cells containing these, useful for recombinant production of the enzyme for use in agricultural waste breakdown and lignocellulostic material treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 871;
                                                  Schuelein M, Olsen AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 871 BP; 283 A; 171 C; 179 G; 238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.7%; Score 634.2; DB 19; Best Local Similarity 97.3%; Pred. No. 6.5e-180; Matches 645; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                      Claim 1; Columns 11-14; 10pp; English
                                                    Bisgard-frantzen H,
             (NOVO ) NOVO-NORDISK AS
                                                                                                          WPI; 1998-376805/32.
                                                                                                                          P-PSDB; AAW60562
                                                    Outtrup H,
                                                                     Dambmann C
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                                                10-MAY-1996;
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The present sequence represents a positive clone for xylanase activity from an example of the present invention. The present invention a describes a novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interest. The method comprises: (i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence and a 3' structural gene sequence; (ii) expressing the resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences encoding a polypeptide with the activity of interest or a related activity, and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms without having to cultivate and isolate the
                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 35; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       Isolating novel DNA sequences from for culturing the microorganism
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Sequence 747 BP; 236 A; 168 C; 154 G; 189 T; 0 other;

밁 Ś 밁 Ś 밁 Ś S 문 밁 S 밁 S 밁 ş 밁 á 밁 S S 문 δ Matches Query Match Match 76.6%; Local Similarity 85.4%; 601 442 361 382 481 421 301 322 241 262 181 202 121 142 566; 61 82 1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAATTCAATGAAACACAAACACAC ATTAACGGTAACCCTCTCTCAACTATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACA 420 TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGATAGT TATTTATGCGTCTATGGTTGGACTGTTGACCCCTCTTGTCGAATATTATATTTGTCGACAGT CAACAAGTTGGTAACATGTCCATAAACTATGGCGCAAACTTCCAGCCAAACGGAAATGCG GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGGAAAATGTATGAAGTCGCG TTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGC TGGGGCAACTGGCGTCCACCAGGGGCAACGCCTAAGGGAACCATCACTGTTGACGGGGG AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAACACAC CAMATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTTGGAAA **AACCACTTTAATGCCTGGGCTGCTCTTGGCATGAATATGGGTGCATTCAATTACCAGATC** TTCAATCAGTACTGGTCGATTCGACAGAGCAAGCGGACCAGCGGCACTGTCACTACGGCA ACGTATGATATCTACAAGCACCAACAGGTCAATCAGCCATCTATTCAGGGCACCGCCACC Conservative <u>,</u> Score 507.8; DB 15; Pred. No. 5e-142; DB 19; Indels Length 0 360 180 120 441 141 60 660 681 600 621 540 480 501 381 300 321 240 261 201

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a DNA encoding xylanase A (XynA) from clostridium stercorarium. XynA contains family VI cellulose binding domain (CBD) which is homologous to the CBD of xylanase D of Xylanase domestridium thermocallum. XynZ is an enzymatic component of C. thermocallum cellulosome and has a multi-domain structure which includes a dockerin domain, a catalytic xylanase domain, a family VI cellulose binding domain and a domain of unknown function. The unknown domain in the N-terminal region of XynZ has been found to contain feruloy! (phenolic acid) esterase which is involved in the degradation of plant cell wall material. The novel feruloyl esterase is thermostable, easy to purify, has high temperature optima and stable over a wide pH range. The anzyme is used for treating grasses or other plant materials used in the pulp and paper
                                                                                                                                                                                                                              Xylanase A; XynA; cellulosome; feruloyl esterase; phenolic acid esterase; thermostable; ferulic acid; wheat bran; agricultural byproduct; treat; grass; paper and pulp industry; feed processing; food additive; plant cell wall material; degradation; ds.
ATTAACGGTAACCCTCTCTCAACTATTAGTAATGACAAGAGCATAACTCTAGATAAAAAC 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA molecule comprising a sequence encoding feruloyl esterase protein, useful for treating grasses and other plant materials used in pulp and paper industries, feed processing and food additives -
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Best Local Similarity
Matches 405; Conserv
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GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
                               GA---CTACGGAAATACGATTATGGAACTTAACGACGGTGGTACTTTTAGTTGTCAATGG
                                                                                       358 GGAACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AGCAACCACTITAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTC
                                                                                                                                                                                                                                                                              TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCAC---TGTTGATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                      418 ACATTTAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTC
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/note= "base n at position 107 is not identified
in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylanase; endo-1,4-beta-D-xylanase; wood pulp; pulpi
biobleaching; bleaching; Bacillus licheniformis; ss.
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/note= "claim 11"
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/note= "claim 12"
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186..266
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Best Local Similarity
Matches 406; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Bacillus pumilus PTL B12 (ATCC 55443) gene library was screened for recombinant plasmids carrying the xylanase gene. A chromosomal fragment obtained from isolate pBPX1 was subcloned and expressed in Escherichia coli JM109. The sequence of the xylanase gene (as a 1022 bp Sau3AI fragment) carried by a selected transformant is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Fig. 1a-1b; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified xylanase from Bacillus pumilus PRL B12 - esp. produced in transformed Bacillus licheniformis, and related DNA, vectors, etc., used for pre-treatment of wood pulp to reduce chlorine or ozone consumption in subsequent bleaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1993;
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for recombinant plasmids carrying the xv
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                                                                                                                                                                                           AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC
                                                                                                                                                                                                                                                                                                       AACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAACACACCAACAAGTTGGT 192
                                                                                                                                                                                                                                                                                                                                                       TCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGGAACAATGTTAAC
                                                                                                                                                                                                                                                                                                                                                                                          GATAATAGGATAGGGACACACAGCGGATACGATTTTGAATTATGGAAGGATTAC---GGA
                     TGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGA
                                                                               TACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATAT
                                                                                                            CGTCCAACAGG---AACGTATAAAGGATCATTTTATGCCGATGGAGGCACATATGACATA
                                                                                                                                    CGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATC
                                                                                                                                                                 TATGGCTGGACACAATCTCCATTAGCTGAATACTACATTGTTGAGTCATGGGGCACATAT
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 TGGAGTGTACGTCAAACAAAACGCACAAGCGGAACGGTCTCCGTCAGTGAGCATTTTAAA
                                                     TATGAAACGCTCCGTGTCAATCAGCCTTCTATCATTGGAGACGCTACCTTCAAACAATAT
                                                                                                                                                                                                                        AACATCTCCATCAACTACAACGCAGCCTTTAACCCGGGGGGAATTCCTATTTATGTGTC
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& CIE.
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/EC_number= 3.2.1.8
/note= "claim 10"
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Pred. No. 3.4e-66;
0; Mismatches 208; Indels
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                                 The present sequence represents a RT46B.1 xynB gene and encodes a xylanae enzyme. The present sequence is derived from a gene contained within Dictyoglomus thermophilum strain Rt46B.1. The xylanase is contained within the family of enzymes known as G-Xylanases, and has beta -1,4-xylanase activity. The enzyme has high activity and high thermal stability with optimum activity at 85 degrees Celcius and pH 6.5. The xylanase enzyme is used for the biological bleaching of cellulose products, especially paper pulp. Use of the enzyme ensures that maste streams from the biological bleaching will include less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xynB gene; xylanse; enzyme; Dictyoglomus thermophilum strain Rt46B G-Xylanase; beta -1,4-xylanase activity; activity; thermal stabilit biological bleaching; cellulose product; paper pulp; ss.
                                                                                                                                                                                               Dictyoglomus thermophilum xylanase gene - used for producing thermally stable enzymes for the bleaching of cellulose products, especially paper pulp
                                                                                                                                                                                                                                                     WPI; 1997-503090/46.
P-PSDB; AAW30267.
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                                                                                                                                                                     Disclosure; Fig 3; 34pp; English.
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                        toxic material
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stability;
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Query Match

Sequence 1190 BP;

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Length 1190;

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                                                            TAGCGGTGGCTCTGGGACAATGATCTCCAATCATGGCGGTACGTTCAGTGCCCAATGGAA 122
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                                        AACACTAACAAGTAATGCAAGCGGTACTTTTGATGGCTACTACTATGAACTATGGAAAGA
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                                                                            TA - - - CAGGGAATACAACCÁTGÁCTGTATÁCACACAAGGATTTAGCTGTCAGTGGAG
                                                                                              CAATGITAACAACATATTACCGTAAAGGTAAAAATTCAATGAAACACAAACACACCA
                                                                                                              CAATATAAACAATGCATTATTCAGAACAGGTAAGAAGTACAAC-----CAAAACTGGCA
                                                                                                                                TITIATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTG
                                                                                                                                                                                   CTTATGTATCTATGGTTGGTCTACTAATCCTTTAGTAGAGTTTTACATTGTAGAAAGTTG
                                                                                                                                                                                                    GGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAAC
                                                                                                                                                                                                                                      ATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATT
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                                                                                                                                                                                                                                                                                                          CCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGGAAAATGTATGAAGTCGCGCT
                                                                                                                                                                                                                                                                                                                            TCACTTTAGGGCATGGGCAAATAGAGGTTTAAACCTTGGTACTATTGATCAAATTACTCT
          Gaps
                                                                                                                                                                                                                                                                                                                                             TACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATAC 593
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delignification; xylan; bleaching; de.
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          Indels
62.4%; Pred. No. 2.9e-53;
ive 0; Mismatches 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
          369; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KONN ) GIST-BROCADES BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xylanase xynD gene.
Similarity
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12-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 TTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAAAGACAAGA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 TTAACAATGCACTCTTCAGAACAGGTAAAAAGTTTAGCACTGCATGGAATCAGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 CATGGCGTCCGCCCGGGGCAACGTCACTTGGCACTGTAACAATTGATGGAGCAACATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 AATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 TCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAAGATAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u> agracricas de recreta a de a de a de a creta e recreta a create a carte a ca</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                 Novel xylanase(s) having activity at 80 deg.C. or higher - obtained from anaerobic thermophilic bacteria and used in paper and pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A full-length xynD gene (AAT08142) codes for a thermostable G-type xylanase (AAR87012) useful in the pulp and paper industries. The gene was obtd. by genomic walking PCR of DNA from an extremely thermophilic bacterium, errain TG456 (CBS 213.94), isolated from a New Zealand hot spring. The gene can be inserted into a vector and used for the prodn. of recombinant xylanase D in microbial host (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17; Length 1244;
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ت
                 Moody D,
Ouax WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
30.9%; Score 204.8; DB 17; Length
Best Local Similarity 61.0%; Pred. No. 4.8e-51;
Matches 367; Conservative 2; Mismatches 224; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1244 BP; 380 A; 215 C; 279 G; 360 T; 10 other;
                 Ś
Forster S,
Morgan HW,
           Iverson S,
Daniel RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Page 56-58; 77pp; English.
     Groenberg V, Williams DP,
Farrel RL, Bergquist PL,
Herweijer MA, Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production processes
                                                                                                                                                                                                                          WPI; 1996-049690/05.
P-PSDB; AAR87012.
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RESULT 12
AAQ92876
ID AAQ92
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                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                    Sequence 164 BP; 50 A; 35 C;
                                                                                                                                                                                                                                                               AAQ92871-77 are examples of several different internal xylanase gene fragments which were used as specific probes to isolate full length cloned genes. AAQ92876 is from an G1-type xylanase. The DNA may be cloned in E. coli using a plasmid vector, and e.g. clone KEX106 was isolated, producing 23.7 U/ml recombinant xylanase. The xylanase may be used in the paper and pulp industries, where it produces an increase in % ISO brightness of softwood pulp of at least 1.0 over non-enzymatically treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg C. The enzyme may be used in production of paper, board and fluff pulp, and has low cellulase activity. The increased brightness produced using the xylanase allows reduction in the amount of bleaching chemicals used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Farrell RL, Goedegebuur F, Herbes WT, Herweijer
Iverson S, Jones BE, Quax WJ, Van Beckhoven RFWC;
Van der Kleij WA, Van Solingen P, Williams DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase chain reaction; Escherichia coli; EC-3.2.1.8; paper; pulp; bleaching; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel xylanase enzyme active at high prodn. processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9518219-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus sp. 1-43-3 (CBS672.93)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermostable alkaline endo-1,4-beta-D-xylanase gene; cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ92876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ92876 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 40-41; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-246385/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable alkaline xylanase gene internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KONN ) GIST-BROCADES NV.
121
                          400
                                                                                    340
                                                                                                                                           280 GAATATTATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGG
                                                        13
                                                                                                                                                                                           Similarity
               TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCG 443
                                                         ACCATCACTGTTGATGGAGGAACATATGATATCTATGAAACTCTTAGAGTCAATCAGCCC
                                                                            GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGA 60
TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGCGTCCG
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                          23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                            0,
                                                                                                                                                                                                                                         39
                                                                                                                                                                            Score 154.4; DB 16
Pred. No. 2.7e-36;
0; Mismatches 6;
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                                                                                                                                                                                                                                       40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PH -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in
                                                                                                                                                                                                        DB 16; Length 164;
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164
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RESULT 13
AAQ92875
ID AAQ92

AAQ92875 standard; DNA; 164 BP

RESULT 14
AAX90405
ID. AAX90

AAX90405

standard;

DNA;

1375

AAX90405;

25-MAR-2003

(updated)

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Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ92871-77 are examples of several different internal xylanase gene fragments which were used as specific probes to isolate full length cloned genes. AAQ92875 is from an G-type xylanase. The DNA may be cloned in E. coli using a plasmid vector, and e.g. clone KEX106 was isolated, producing 23.7 U/ml recombinant xylanase. The xylanase may be used in the paper and pulp industries, where it produces an increase in $ ISO brightness of softwood pulp of at least 1.0 over non-enzymatically treated pulp in an ECF pulp bleaching process, at pH 9.0 and 65 deg C. The enzyme may be used in production of paper, board and fluff pulp, and has low cellulase activity. The increased brightness produced using the xylanase allows reduction in the amount of bleaching chemicals used.
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Iverson S, Jones
Van der Kleij WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 164 BP; 50 A; 35 C; 39 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Page 40; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-246385/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KONN ) GIST-BROCADES
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
121
                                                            400
                                                                                                                                                                                                   340
                                                                                                                                                                                                                                                                                                                                   280 GAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGG 339
                                                                                                                                                                                                                                                                                                                                                                                                      156;
                                                                                                                               61
                                                                                                                                                                                                                                                                   μ
                                                                                                                                                                              TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCG 443
                                                                                                                        ACCATCACTGTTGATGGAGGAACATATGATTACTATGAAACTCTTAGAGTCAATCAGCCC
                                                                                                                                                                                                                                                                   GAATATTATATTGTCGACAGTTGGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGA
TCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGCGTCCG 164
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goedegebuur F, Herbes WT, Herweijer MA,
Jones BE, Quax WJ, Van Beckhoven RFWC;
j WA, Van Solingen P, Williams DP;
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95.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 151.2; DB 16; pred. No. 2.5e-35; 0; Mismatches 8;
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    useful in

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TTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCC

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608 GACCGTGACCTACAACGCCTCCTTCAACCGGTCGGGTAACGGCTACCTCACGCTCTACGG 667
                                                 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a culture medium obtained from the culture of a recombinant host cell that is not Actinomadura flexuosa and has been transformed with a vector encoding a protein having xylanase activity, where the protein comprises an amino acid sequence from a xylanolytic fragment of the amino acid sequence in AAY24480 or AAY24481. The enzyme composition can be used in a method for biobleaching, modifying plant biomass properties, especially the reduction of lignin content in pulp and paper processing. The xylanases are hemicellulases which partially degrade the hemicellulose and enhance the extractability of lignins by conventional chemical bleaching of wood pulp. It can be used alone or as a supplement to other treatments that reduce lignin content of wood pulp, increase its drainability or decrease its water retention. The culture medium can be used directly without the need to purify the enzymes. Actinomadura flexuosa xylanases have a pH optimum the need to acidify the pulp prior to xylanases treatment. The xylanases partially degrade the hemicellulose in wood pulp which enhances the extractability of lignins by conventional bleaching chemicals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formation of environmentally undesired organic compounds. The present sequence encodes Actinomadura sp. DSM43186 35 kDa xylanase. N.B. This sequence is indexed from US5935836 which is a treat as
                                                            Actinomadura sp. DSM41186; xylanase; Actinomadura flexuosa; lignin; thermostable; biobleaching; wood pulp; bleaching; hemicellulase; paper processing; hemicellulose; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     results in a lower consumption of bleaching chemicals reducing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomadura xylanase sequences and method of use. - No abstract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maentylae A;
                                Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1375 BP; 265 A; 517 C; 400 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lantto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Updated on 25-MAR-2003 to correct DR field.)
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                                                                                                                                                                                          /*tag= a
/product= "xylanase"
                                                                                                                                                        Location/Qualifiers
303..1337
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                          (ALKO-) ALKO GROUP LTD.
(ALKO-) ALKO-YHTIOET OY.
(ROHG ) ROEHM ENZYME FINLAND OY.
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94US-0332412.
95FI-0003639.
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Suominen P,
(first entry)
                                                                                                                         Actinomadura flexuosa.
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                                                                                                                                                                                                                                                                                                 06-JUN-1995;
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28-SEP-1999
                                                                                                                                                                                                                                     US5935836-A.
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497
318 ACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATTTTTACGA 377
                                                                     728 cacces---caccracaagggacaccarcaccaccgacgggaacgracgacarcracga 784
                                                                                                    378 GACTCTTAGAGTCAATCAACCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAG 437
                                                                                                                                  785 GACCTGGCGGTACAACGCGCCCTCCATCGAGGCACCCGGACCTTCCAGCAGTTCTGGAG 844
                                                                                                                                                                                                845 CGTCCGGCAGCAGAGCGGACCAGCGCCATCACCATCGGCAACCACTTCGACGCTG 904
                                                                                                                                                                                                                              498 GGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTA 557
                                                                                                                                                                                                                                                             905 GGCCCGCGCCGCATGAACCTGGGCAGCCACGACTACCAGATCATGGCGACCGAGGGCTA 964
                                                                                                                                                                                                                                                                                                             965 CCAGAGCAGCGGTAGCTCCCACCGTCTCCATCAGCGAGGGTGGCAACCCCGGCAACCC 1021
                                                                                                                                                                                                                                                                                            558 TCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGAATTAACGGTAACCC 614
                                                                                                                                                                 | TGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomadura flexuosa; xylanase; cellulase; recombinant; fungal host; pulp; paper industry; enzyme; bleaching; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lahtinen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of bacterial proteins, especially xylanase(s) and cellulase(s) - by recombinant expression in a filamentous fungal host, useful particularly in the pulp and paper industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomadura flexuosa 35 kDa (AM35) xylanase encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lantto R, Fagerstroem R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "AM35 xylanase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Pages 65-67; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           AAT64930 standard; DNA; 1375 BP.
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Vehmaanperae J;
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432..1334
/*tag= b
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(first entry)
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02-APR-1998
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                                                                                                                                                                 438
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3; Gaps

DB 17; Length 1375;

Score 119.4; DB 17; Length Pred. No. 2.1e-25; 0; Mismatches 176; Indelè

18.0%; 57.1%;

Query Match Best Local Similarity 57.14 Matches 238; Conservative

CC This DNA encodes the Actinomadura flexuosa 35 kDa (AM35) xylanase. The CC bacterial protein xylanase can be produced by a recombinant expression CC vector in a filamentous fungal host. The vector comprises a promoter CC operably linked to a DNA sequence of a filamentous fungus secretable CC protein or one or more functional domains of the protein, which is fused CC in frame with a DNA sequence encoding the bacterial protein, which is fused CC expression vector is used particularly for the production of bacterial proteins and enzymes, especially xylanases and cellulases. The enzyme CC proteins are very economical to provide and use. Isolation of a specific enzyme from the culture fluid is unnecessary because the carymes may be used in a crude form. As the enzymes are secreted into the desired enzyme preparation, and there is no need to extract an enzyme CC from the hosts. The Actinomadura flexuosa xylanases have a pH optimum and CC thermostability that are desirable for enzyme aided bleaching of wood CC pulp. The bacterial xylanases can be used in the pulp and paper industry ce.g. enzyme-enhanced bleaching of paper making pulp, enzymatic CC fiberisation during beating, enzymatic increase of drainage rates and ink CC envolation during beating, enzymatic plant biomass.

(Updated on 25-MAR-2003 to correct PI field.) Query Match 18.0 Best Local Similarity 57.1 Matches 238; Conservative Sequence 1375 BP; 265 A; 517 C; 400 G; 193 T; 0 other; 965 CCAGAGCAGCGGTAGCTCCACCGTCTCCATCAGCGAGGGTGGCAACCCCGGCAACCC 1021 558 905 498 845 438 785 378 728 318 ACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGA 377 668 258 TTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCC 317 608 GACCGTGÁCCTÁCAACGCCTCCTTCAÁCCCGTCGGGTÁÁCGGCTÁCCTCACGCTCTÁCGG 198 GTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGG 257 GACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAG 437 TCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGAATTAACGGTAACCC 614 GGCCCGCGCGCATGAACCTGGGCAGCCACGACTACCAGATCATGGCGACCGAGGGCTA 964 GGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTA 557 CGTCCGGCAGCAGAAGCGGACCAGCGGCACCATCACCATCGGCAACCACTTCGACGCCTG 904 TGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTG 497 GÁCCTGGCGGTACAACGCGCCGTCCATCGAGGGCACCCCGGACCTTCCAGCAGTTCTGGAG 844 CACCGG---CACCTACAAGGGCACCGTCACCACCGACGGGGAACGTACGACATCTACGA CTGGACCAGGAACCCGCTCGTCGAGTACTACATCGTCGAGAGCTGGGGCACCTACCGGCC 18.0%; Score 119.4; DB 18; Length 1375; 57.1%; Pred. No. 2.1e-25; ative 0; Mismatches 176; Indels 3; 3; Gaps 1 784 727 667 1;

Search completed: October 20, 2003, 11:27:58 Job time: 262 secs

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October 20, 2003, 10:40:37 ; Search time 2552 Seconds (without alignments) 10628.167 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-909-207-1 663 1 CABATCGTCACCGACAATTC.....TAACTTTGGATAAAAACAAT 663 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2888711 segs, 20454813386 residues Total number of hits satisfying chosen parameters: Searched:

5777422

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB ID 663 6 A8822 A88222 663 100.0 663 6 A8822 663 100.0 744 6 A8822 663 100.0 744 6 A8822 663 100.0 744 6 A8822 663 100.0 1513 6 A8821	Accore Match Length DB ID 663 100.0 663 6 A48222 663 100.0 663 6 A48222 663 100.0 663 6 A48222 663 100.0 663 6 A48225 663 100.0 663 6 A48225 663 100.0 744 6 A48225 663 100.0 744 6 A48225 663 100.0 744 6 A48231 663 100.0 744 6 A48231 663 100.0 1513 6 A48231 664 100.0 1513 6 A48231 674.2 95.7 744 6 A813130 674.2 95.7 744 6 A813130 674.2 95.7 744 6 A81313 675.2 53.6 1531 1 A802031 676.4 4 2.3 1 454 1 CLOXYNB 676.4 4 2.3 1 454 1 CLOXYNB 677.4 4 42.3 1 454 1 CLOXYNB 678.4 4 2.3 1 17 577 1 1 A8010958 678.2 4 38.5 1022 6 A4225 675.2 38.5 1022 6 A4221306 675.2 38.5 1022 6 A4221306 675.2 38.5 1022 6 A8221306 675.2 38.5 600 6 A42204 675.3 38.5 600 6 A8220045	1		de			SUMMARIES	
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De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof
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Xylanase, microorganisms for its production, DN
of preparation and use thereof
Patent: EP 0698667-A 2 28-FEB-1996;
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 100870 960604
Other publication BE 9503454 960305
Other publication BR 9503478 960127
Other publication FI 953578 960127
Other publication AU 2508695 960208.
Location AU 2508695 960208.
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NWRPPGATPKGTITVDGGTYDIYETLRVNQPSIKGIATFKQYMSVRRSKRTSGTISVS
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conflict with the conceptual translation"
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/db_xref="taxon:32644"
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Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JP 8092284 960409
Other publication PI 953578 960127
Other publication CA 2154628 960127
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Mismatches 0;
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Xylanase, microorganisms for its production, DN
of preparation and use thereof
Patent: EP 069867-A 5 28-FEB-1996;
SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 100870 960604
Other publication BE 9503454 960305
Other publication FB 9503454 960127
Other publication FJ 8092284 960127
Other publication CA 2154628 960127
Other publication AU 2508895 960208.
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1. .81
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De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods ipreparing this xylanase and uses of the latter
Patent: US 6346407-A 5 12-PEB-2002;
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144 c 160 g
                                                      Query Match
Best Local Similarity 100.0%;
Matches 663; Conservative 0
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De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
Patent: US 6346407-A 4 12-FEB-2002;
Location/Qualifiers
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cal Similarity 100.0%; Pred. No. 1.5e-169;
.663; Conservative 0; Mismatches 0;
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Other publication BE 1008751 960702
Other publication BE 1008570 960604
Other publication BR 9503454 960305
Other publication JR 9503454 960305
Other publication FI 953578 960127
Other publication CA 2154628 960127
Other publication AU 2508695 960208.
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De Buyl, E., Lahaye, A., Ledoux, P. and Detroz, R.
Xylanase, microorganisms producing it, DNA molecules, methods for preparing this xylanase and uses of the latter
Patent: US 6346407-A 10 12-PEB-2002;
Location/Qualifiers
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S De, B.E., Lahaye, A., Ledoux, P. and Detroz, R.

Kylanase, microorganisms for its production, DNA molecules, process of preparation and use thereof

L Patent: EP 0698667-A 11 28-FEB-1996;

SOLVAY (BE)
Other publication BE 1008751 960702
Other publication BE 1008751 960604
Other publication BR 9503454 960305
Other publication FI 953578 960127
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Patent: US 6346407-A 11 12-FEB-2002;
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                                               TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
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Dalboege, H., Diderichsen, B., Sandal, T. (METHOD OF PROVIDING MOVEL DNA SEQUENCES Patent: WO 9743409-A 1 20-NOV-1997;
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              GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
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AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAATTCAATGAAACACAAAACACAC
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SIKGIAIFKQYMSVRSKRTSGTISVSNHFRAMENLGNNMGKMYEVALTVEGYQSSGS
ANVYSNTLRINGNPLSTISNDKSITLDKNN"
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Van, S.P., Williams, D.P., Iverson, S., Farrell, R.L., Herbes, W.T.,
Van, S.P., Williams, D.P., Iverson, S., Farrell, R.L., Herbes, W.T.,
Jones, B.E.
ALKALI-TOLERANT XYLANASES
Patent: WO 9518219-A 18 06-JUL-1995,
GIST BROCADES VO NL)
Other publication JP 8507221T 960806
Other publication NO 95312 951019
Other publication NO 95312 951019
Other publication FI 95392 950821
Other publication AU 1415095 950717.
  202 AACAATGTTAACAACATATTATTCGGTAAAGGTAAAAATTCAATGAAACACAACACAC 261
                                           361 ACATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACA
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A45313.1 GI:2299796
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Unclassified.

(Dases 1 to 744)

Dalb.o slashed.ge,H., Sandal,T., Kauppinen,M.Sakari. and
Diderichsen, Bslashedrge.
Method of providing a hybrid polypeptide exhibiting an activity of interest
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CAACAAGTTGGTAACATGTCCATAAACTATGGCGCAAACTTCCAGCCAAACGGAAATGCG
                                                                                                            TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
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95.7%; Score 634.2; DB 6; Length
Best Local Similarity 97.3%; Pred. No. 1e-161;
Matches 645; Conservative 0; Mismatches 18; Indels
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Seguence 1 from patent US 6270968.
AR163110
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/translation="MSQKKLTLINLFSLFALTLPARISQAQIVTDNSIATRGGYDYEF WKDSGGSGTMILNHGGTFSAQWNNVNNILFRKGKKFNETQTHQQVGNMSINYGANFQP NGNAYLCYYGWTVDFLVBYYIVDSMGNWRPPGATFKGTITVDGGTYDIYETLRVNQPS IKGIATFKQYWSFRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGSA NYYSNTLRINGNPLSTISNNESITLDKNN"

148 a 145 c 159 g 192 t

	Search completed: October 20, 2003, 11:23:26	Search con Job time
	739 AAT 741	망
	661 AAT 663 .	Ş
	679 ATTAACGGAAACCCTCTCTCAACTATTAGTAATAACGAGAGCATAACTCTAGATAAAAAC 738	Db dd
	601 ATTAACGGTAACCCTCTCTCAACTAATTAGTAATGACGAGAGCATAACTTTGGATAAAAAC 660	Ş
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	541 CTTACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGA 600	ई
	559 AACCACTTTAGAGCGTGGGAAAAACTTAGGGATGAACATGGGGAAAATGTATGAAGTCGCG 618	망
	481 AACCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAAATGTATGAAGTCGCG 540	Ş
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	301 TGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA 360	Ś
	319 TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTTGAATATTATATTGTCGACAGT 378	Db
	241 TATTTATGCGTCTATGGACTGTTGACCCCTCTTGTCGAATATTATATTTGTCGACAGT 300	Ş
	259 CAACAAGTTGGTAACATGTCCATAAACTATGGCGCAAACTTCCAGCCAAACGGTAATGCG 318	дb
3	181 CAACAAGTTGGGTAACATGTCCATAAACTACGGAGCCAACTTCCAACCAA	Ą
	199 AATAATGTTAACAATATATTATTCCGTAAAGGTAAAAAATTCAATGAAACACAAACACAC 258	ğ
	121 AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAATTCAATGAAACACAAACACAC 180	Ş
	139 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 198	В
	61 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG 120	Ş
	79 CAAATCGTCACCGACAATTCCATTGCCACCGGGTGGTTATGATTATGAATTTTTGGAAA 138	Db
	1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA 60	Ş
	y Match 94.2%; Score 624.6; DB 6; Length 744; Local Similarity 96.4%; Pred. No. 4.2e-159; hes 639; Conservative 0; Mismatches 24; Indels 0; Gaps 0;	Query Ma Best Loo Matches
	T 248 a 145 c 159 g 192 t	BASE COUNT ORIGIN
	TKGTATFKOYWSVRRSKRTSGTTSVSNHFRAWENI.GMNMGKMYEVALITVEGYOSSGSA	

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	October 20, 2003, 11:28:06; Search time 1595 Seconds (without alignments) 1091.613 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-909-207-1 663 1 CAATCGTCACCGACAATTCTAACTTTGGATAAAACAAT 663
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	1750203 segs, 1313063994 residues
Total number of	Total number of hits satisfying chosen parameters: 3500406
Minimum DB seq length: 0	Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: Published Applications NA:*

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 1, Appli	Sequence 2, Appli	4	Sequence 5, Appli	ä	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 39, Appl	Sequence 71, Appl	Sequence 70, Appl	68,	Sequence 1, Appli	Sequence 64, Appl	65,	Sequence 67, Appl
	ID .	US-09-909-207-1	US-09-909-207-2	US-09-909-207-4	US-09-909-207-5	US-09-909-207-10	US-09-909-207-11	US-09-770-621-1	US-10-286-993-1	US-10-307-441-39	US-10-213-990-71	US-10-213-990-70	US-10-213-990-68	US-10-299-393-1	US-10-213-990-64	US-10-213-990-65	US-10-213-990-67
	DB	12	10	10	10	10		σ		12	14	14	14	14	14	14	14
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de	Query Match Length DB	100.0	100.0	100.0	100.0	100.0	100.0	18.0	18.0	17.4	16.8	16.6	16.4	16.0	15.8	15.6	14.6
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TELEFAX: (202) 293-1850

Sequence 3, Appli	10,	Sequence 11, Appl	8,	Sequence 9, Appli	٦,	Sequence 5, Appli	39,	24,	Sequence 1, Appli	Sequence 793, App	Seguence 308, App		Sequence 2116, Ap		Sequence 2, Appli	6	Seguence 297516,	Sequence 170, App	Seguence 212128,	Seguence 9387, Ap	Sequence 1, Appli	Sequence 199892,	Sequence 199893,	1872	Sequence 701, App	Sequence 1405, Ap	Sequence 1, Appli	Seguence 2141, Ap
US-09-803-454-3	US-10-237-386-10	US-10-237-386-11	US-09-790-070A-8	US-10-237-386-9	US-09-467-368-1	US-10-419-969-5	US-10-340-860A-39	US-10-307-441-24	US-09-970-616-1	US-10-311-455-793	US-10-311-455-308	US-10-027-632-13285	US-10-311-455-2116	US-09-840-743-10	US-10-312-841-2	US-10-027-632-63151	US-10-027-632-297516	US-08-781-986A-170	US-10-027-632-212128	US-10-027-632-9387	US-09-792-616-1	US-10-027-632-199892	US-10-027-632-199893	US-10-311-455-1872	US-10-311-455-701	US-10-311-455-1405	US-10-312-841-1	US-10-311-455-2141
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13.1	12.5	12.5	11.9	10.9	10.9	8.2	7.6	6.2	6.0	5.7	5.7	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.2	5.2	5.2	5.5
86.8	83.2	83.2	79	72.4	72.4	54.2	50.4	41	40	38	37.6	36	36	35.8	35.8	35.6	35.6	35.6	35.2	35.2	35.2	35	35	35	34.8	34.8	34.8	34.6
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ALIGNMENTS

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RESULT 2
US-09-909-207-2
                                Sequence 2, Application US/09909207
Patent No. US20020115181A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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SEQUENCE DESCRIPTION: SEQ ID NO:
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                   APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
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ilarity 100.0%;
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Pred. No. 3.1e-186;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..663
SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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FILING DATE: 19-Jul-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSE: WILLIAN BRINKS HOFER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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LOCATION:
TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTTGTCGACAGT
                                                     GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
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TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 06-JUNE-1995
                                                                                                                        AACAATGTTAACAACATATTATTCCGTAAAGGTAAAAAATTCAATGAAACACAAACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-429-0625
TELEFAX: (202) 293-1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4121-40
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RENE DETROZ
INVENTION: Xylanase, microorganisms produced it,
DNA molecule, processes for preparation
and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
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Pred. No. 3.1e-186;
; Mismatches 0;
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                                                                                                                                                                           Query Match 100.0%; Score 663; DB 10; Best Local Similarity 100.0%; Pred. No. 3.3e-186; Matches 663; Conservative 0; Mismatches 0;
                                                                                                     STRAIN: Bacillus
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09909207; Patent No. US20020115181A1; GENERAL INFORMATION:
                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ERIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
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US-09-909-207-4
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DNA molecule, processes for preparation of this xylanase
and uses thereof
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241 TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTTGTCGACAGT 300
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                                 TGGGGCAACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
CITY: Washington STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
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COMPUTER: IBM PC COMPALIble
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
FILING DATE: 19-JU1-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Wilhlem F. Gadiano, Esq. REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
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FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Patent No. US20020115181A1
GENERAL INFORMATION:
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US-09-909-207-4
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; NAME/KEY: sig_peptide
; LOCATION: 1..81
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-909-207-5
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PILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAWE: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-0625
TELEPHONE: 202-429-0625
TELEPAX: (202) 293-1850
TELEPAX: (50) 383-5605
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 663; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHORIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,207
PILING DATE: 19-701-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIONE
STREET: 2000 K St., N.W., Suite 200
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ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                   202 AACAATGTTAACAACATATTATTCCGTAAAAGGTAAAAAATTCAATGAAACACAAACACAC
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                                                                                                                                                                                                                                       61 GATAGCGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCAATGG
                                                                                                                                                                                                                                                                                         82 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA 141
                                                                                                                                                                                                                                                                                                                 1 CAAATCGTCACCGACAATTCCATTGGCAACCACGATGGCTATGATTATGAATTTTGGAAA
TATTTATGCGTCTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGT
                                                                                   LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 82..744
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LOCATION: 1..744
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Pred. No. 3.3e-186;
D; Mismatches 0;
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US-09-909-207-10
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                     TELEX: 650 383-5605 INFORMATION FOR SEQ ID NO: 10:
                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/99/909,207
FILING DATE: 19-Jul-2001
CLASSIFICATION: c'Onknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,953
FILING DATE: 06-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REFERRICE/DOCKET NUMBER: 37,136
REFERRICE/DOCKET NUMBER: 4121-40
TELEPHONE: 202-429-0625
TELEPHONE: 202-429-0625
TELEPHONE: (202) 293-1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIONE STREET: 2000 K St., N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Xylanase, microorganisms produced it,

DNA molecule, processes for preparation of this xylanase
and uses thereof
   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ANDREE LAHAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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PIERRE LEDOUX
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DNA molecule, processes for preparation of this xylanase and uses thereof correspondence: 29

CORRESPONDENCE ADDRESS: 28

ADDRESSEE: WILLIAM BRINKS HOFER GILSON & LIONE CITY: Washington STREET: 2000 K St., N.W., Suite 200

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 2000
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MEDIUM TYPE: FLORPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/909,207

FILING DATE: 19-Jul-2001

CLASSIFICATION NUMBER: 08/470,953

PILING DATE: 06-JUNE-1995

ATPORNEY/AGENT INFORMATION:

NAME: Wilhlem F: Gadiano, Esq.

REGISTRATION NUMBER: 37,136

REGISTRATION NUMBER: 37,136

REGISTRATION NUMBER: 4121-40

TELECAMINICATION INFORMATION:

TELECAMINICATION NUMBER: 4121-40

TELECAMINICATION NUMBER: 37,136

REGISTRATION NUMBER: 37,136

TELECAMINICATION NUMBER: 31,136

REGISTRATION NUMBER: 31,136

TELECAMINICATION NUMBER: 31,136

TELECAMINIC
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Similarity 100.0%; Pred. No. 4.8e-186;
33; Conservative 0; Mismatches 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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LOCATION: 701..1363
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STRANDEDNESS: single
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LOCATION: 620..1363
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BRIC DE BUYL
PIERRE LEDOUX
RENE DETROZ
TITLE OF INVENTION: Xylanase, microorganisms produced it,
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                 ; Score 663; DB 10;
; Pred. No. 4.8e-186;
0; Mismatches 0;
                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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Patent No. US20020115181A1
GENERAL INFORMATION:
                                                                                                                  LENGTH: 1513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 663; Conservative 0;
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US-09-909-207-11
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Sequence 1, Application US/09770621
Patent No. US20010024815A1
GENERAL INFORMATION:
APPLICANT: M ntyl , Arja
APPLICANT: Vehmaanper , Jari
APPLICANT: Fagerstr m, Richard
APPLICANT: Lantto, Raija
APPLICANT: Paloheimo, Marja
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US-09-770-621-1
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APPLICANT: Lahtinen, Ta:
TITLE OF INVENTION: PRO-
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
PILING DATE: 31-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New 1
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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APPLICATION NUMBER:
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FILING DATE:
CLASSIFICATION:
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CLASSIFICATION:
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Suominen, Pirkko
Lahtinen, Tarja
NVENTION: Production &
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US-09-770-621-1
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Best Local Similarity
Matches 238; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1375 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. US20010024815A1 Relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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CCAGAGCAGCGGTAGCTCCACCGTCTCCATCAGCGAGGGTGGCAACCCCGGCAACCC 1021
                                                                                                                                                 CGTCCGGCAGCAGAGCGGACCAGCGGCACCATCACCATCGGCAACCACTTCGACGCCTG
                                                                                                                                                                                      TGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTG
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                               TCAAAGTAGCGGAAGTGCTAATGTATATAGCAATACACTAAGAATTAACGGTAACCC 614
                                                                      GGCCCGCGCCGGCATGAACCTGGGCAGCCACGACTACCAGATCATGGCGACCGAGGGCTA
                                                                                                           GGAAAACTTAGGGGATGAATATGGGGAAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTA 557
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ilarity 57.1%;
Conservative
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Pred. No. 8.2e-25;
0; Mismatches 176;
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US-10-286-993-1
US-10-286-993-1
Sequence 1, Application US/10286993
Publication No. US20030148453A1:
GENERAL INFORMATION:
APPLICANT: Mantyla, Arja
APPLICANT: Lantto, Raija
APPLICANT: Lantto, Raija
APPLICANT: Lanttonen, Tarja
APPLICANT: Suominen, Pirkko
APPLICANT: Suominen, Pirkko
APPLICANT: Vehmaanpera, Jari
TITLE OF INVENTION: Production and Secretion of Proteins
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in

Filamentous

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253
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APPLICANT: SING, Wing L.
APPLICANT: SING, Wing L.
APPLICANT: SING Wing L.
APPLICANT: SING Wing L.
APPLICANT: SING Wing L.
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
TITLE OF INVENTION: and Alkalophilicity
TITLE OF INVENTION: and Alkalophilicity
FILE REFERENCE: 027367-506US
CURRENT PAPLICATION NUMBER: US/10/307,441
CURRENT FILING DATE: 2001-15-31
PRIOR FILING DATE: 2001-05-31
PRIOR PLING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 39
LENGTH: 596
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                                                                                                                                                                                                                                                                     Length 1375;
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                                                                                                                                                                                                                                                                 Score 119.4; DB 12; Length
Pred. No. 8.2e-25;
0; Mismatches 176; Indels
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PRIOR APPLICATION NUMBER: US 08/590,563
PRIOR FILING DATE: 1996-01-26
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 1375
TYPE: DNA
ORGANISM: Actinomadura flexuosa (Strain: DSM43186)
PRATURE:
NAME/KEY: CDS
                                                                                                                                                                               ; LOCATION: (303)..(1337)
; OTHER INFORMATION: Product= AM35 xylanase
US-10-286-993-1
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Best Local Similarity 57.1%;
Matches 238; Conservative
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ORGANISM: Artificial Sequence
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Sequence 71, Application US/10213990
Fublication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: J0108
APPLICANT: Bussey, Howard
APPLICANT: Storma, Reg
APPLICANT: Storma, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: NUCLEIC ACIDS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION UNMER: 2012-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FalcSEQ for Windows Version 4.0
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                                                                                                                             193 AACATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTC
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Score 115.2; DB 12; Length 596;
Pred. No. 9.3e-24;
0; Mismatches 163; Indels 3;
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Pred. No. 1.6e-22;
0; Mismatches 166; Indels 3;
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Query Match 17.4%;
Best Local Similarity 57.7%;
Matches 226; Conservative C
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Best Local Similarity 57.0%;
Matches 224; Conservative
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ORGANISM: Aspergillus
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, LOCATION: (1)...(942)
US-10-213-990-71
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GENERAL INFORMATION:

APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Rosmer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION OF SEQ ID NOS: 72
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 70
LENGTH: 1002
TYPE: DNA
ORGANISM: Aspergillus
US-10-213-990-70
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US-10-213-990-70
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                                     TCAAAGTAGCGGAA 571
                                                                                                           GGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTA
                                                                                                                                                                                   TGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTG 497
                                                                                                                                                                                                                                                              GACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCTTACTGTAGAAGGCTATCAAAGTAGCGGAA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAATCACTTCAAGGCCTGGGCTAGTCTGGGGATGAACCTGGGTACCCATAACTATCAGA 616
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                                                                                                                                                  CATCCGCCAAAACAAGCGATCCAGCGGCACAGTCACCACCGCGAATCACTTCAAGGCCTG
                                                                                                                                                                                                                          GCACCAACAGGTCAACCAGCCTTCGATCGTCGGCACGGCCACCTTCAACCAATACTGGTC
                                                                          GGCTAGTCTGGGGATGAACCTGGGTACCCATAACTATCAGATTGTTTCCACTGAGGGATA
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US-10-213-990-68
                                                                      문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 68, Application US/10213990 Publication No. US20030082595A1 GENERAL INFORMATION:
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Aspergillus FEATURE: NAME/KEY: CDS LOCATION: (1)...(705)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
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nes 298; Conserv
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                            TACTGTAGAAGGCTATCAAAGTAGCGGAAGTGCT
                                                                                                                                               CACCCAGTACTGGTCTGTGCGCACCTCCAAGCGTACCGGCGCACTGTCACCATGGCCAA
                                                                                                                                                                               TAAACAATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAA 482
                                                                                                                                                                                                                     ATATGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATT
                                                                                                                                                                                                                                                                                            TACATACAACCCCGGCAGCGGCGCTACCTTCAGGGGCACTGTCAACACCGACGGTGGCAC
                                                                                                                                                                                                                                                                                                                              CA---ACTGGCGTCCACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                    GGCTGTCTACGGCTGGACCACCAACCCCTTGATTGAGTACTACGTTGTTGAGTCGTATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTGGCTCTGGGACAATGATTCTCAATCATGGCGGTACGTTCAGTGCCCCAATGGAACAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCACCCCAAGCTCCACCGGCTGGAACAACGGCTACTACTACTCCTTCTGGACTGATGG
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 CGCCACTGAGGGTTACCAGAGCAGCGGATCTGCT 687
                                                                        CCACTTCAACGCCTGGAGCAGACTGGGCATGAACCTGGGAACTCACAACTACCAGATTGT
                                                                                                        CCACTTTAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAAATGTATGAAGTCGCGCT
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108.8; DB 14; Length 705;
Pred. No. 8e-22;
0; Mismatches 267; Indels 9;
                                  576
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RESULT 13 US-10-299-393-1 ; Sequence 1, Application US/10299393

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; Sequence 65, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
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     Publication No. US20030082595A1
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.8°
Matches 221; Conservative
                                                                                                                                                                                                                                                                                                             , ORGANISM: Aspergillus
US-10-213-990-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 CATGTCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTA
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                                                   APPLICANT: Fish, Neville Marshall
APPLICANT: Haigh, Nigel Paterson
TITLE OF INVENTION: PENTICLILIUM FUNICULOSUM STRAIN USEFUL
TITLE OF INVENTION: PENTICLILIUM FUNICULOSUM STRAIN USEFUL
TITLE OF INVENTION: POR THE PRODUCTION OF ENZYMES
FILE REFERENCE: A32917-PCT-USA-I (072667.0183)
CURRENT APPLICATION NUMBER: US/10/299,393
CURRENT PILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: EPO 9801161.5
PRIOR APPLICATION NUMBER: EPO 9801161.5
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.0%; Score 106; DB 14; Length 2 Best Local Similarity 56.5%; Pred. No. 1.1e-20; Matches 218; Conservative 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000 AGGCTACGAGAGCAGTGGCTCTAGTA 2025
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                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Penicillium funiculosum
Publication No. US20030108642A1
GENERAL INFORMATION:
APPLICANT: Sabatier, Alain
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (1317)...(1589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
(1644)...(2042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1590) ... (1642
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LOCATION: (724)...(730)
US-10-299-393-1
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LOCATION: (570)...(576)
FEATURE:
                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 2898
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NAME/KEY:
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; Sequence 64, Application US/10213990

RESULT 14 US-10-213-990-64

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APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: BAZYMES AND METHODS OF USB
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT APPLICATION NUMBER: US/10/213,990
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PASLESQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 666
GENERAL INFORMATION:

APPLICANT: Jang, Bo
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: BUZYMES AND METHODS OF USE
TITLE REFERENCE: 10182-019-599
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 cereraceceredaceaceaerececrecicearreracarecrecaeaerracecre 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 CAACCICTACAAGACGACGCGGACGAATGCGCCGTCCATCCAGGGCACGGCTACTTTTGA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 ccaeracregregerregacrregeacecegeagagagacrergacgacgagagagea 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604 CTTTGATGCGTGGAGAAATGCGGGTCTGCAATTGGGGAACTTTGACTATATGATTGTTGC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 TGATATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 104.8; DB 14; Length
Pred. No. 1.2e-20;
0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   546 TGTAGAAGGCTATCAAAGTAGCGGAAGTGCTAATGT 581
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ORGANISM: Aspergillus
FEATURE:
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; LOCATION: (1)...(666)
US-10-213-990-65
Search completed: October 20, 2003, 13:35:44 Job time : 1600 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 CTCTTAGAGTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 CGGGAGCCACCCATCTCGGCACCGTCGAGAGCGACGGGGCCACGTACAACCTCTACAAGA 451
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                                                                                                                           632 AGAGCAGCGGCTCTGCTACTAT 653
                                                                                                                                                              560 AAAGTAGCGGAAGTGCTAATGT 581
                                                                                                                                                                                                                                                    572 GAAATGCGGGTCTGCAATTGGGGAACTTTGACTATATGATTGTTGCGACGGAGGGGTACC 631
                                                                                                                                                                                                                                                                                                          500 AAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATC 559
                                                                                                                                                                                                                                                                                                                                                                      512 TTCGGACTTCGCACCGGCAGAGTGGAACTGTGACGACGAAGAACCACTTTGATGCGTGGA 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 TCACCTACAGCGGCTCCTGGCAGACCAGCGGAAACGGCTACCTCTCCGTGTACGGCTGGA 331
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Scoring table:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Run

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Scribm bicolor (Borghum)
Sorghum bicolor (Borghum)
Sorghum bicolor (Borghum)
Sorghum bicolor (Sorghum)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyte; Liliopsida; Poales; Poacese; PACCAD clade; Panicoidese; Andropogoneae; Sorghum.

In (Dases 1 to 738)
Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chua Tan , N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid (ACC)-treated seedlings
               AQ160254 mgxb00031

AQ35244 mgxb0001B

AQ399120 mgxb0010B

AQ48084 mgxb0010B

AQ48084 mgxb0010B

AQ398756 mgxb0010B

BQ165950 WHE0821-0

BQ165950 WHE0821-0

BQ156480 WHE0821-0

BM1349078 wHE0821-0

BM1349078 wHE0821-0

BM135798 WHE0821-0

BM135798 WHE082-1

AC63020 WCI-11-4

CA447770 UI-H-EIO-1

BC02233 MMS muscu

BC110128 VD0103B07

BC110128 VD0103B07

BC110128 VD0103B07

AC63020 RCI-11-4

CA447770 UI-H-EIO-1

BC102233 MMS muscu

BC110128 VD0103B07

AC63020 RCI-11-4

CA447770 UI-H-EIO-1

BC10233 MS muscu

BC110128 VD0103B07

AC63020 RCI-11-4

CA447770 UI-H-EIO-1

BC102333 MS muscu

BC1023911 AV315991

BH938430 Odf67f12.

CL160658 K-EST0220

AL106776 DC00Bbh11

BC102377 yx57406-61

BH989520 Ocem8590-1

AG007299 HOMC SBP1

AG007209 HOMC SBP1

BC062201 HQ314900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
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                                                                                                                                                                                                       AQ449078
BF200865
BOT50865
BOT508654812
CD033274
BBM135798
BBM135798
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BM1010128
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AM0530020
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AG007299
AG007300
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 38.8
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AUTHORS
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CD464145 ETH1 48 B
CD458837 FG08 0451
AQ160513 mgxb0006C
AQ447125 mgxb0005C
                                                                                                                          October 20, 2003, 10:40:41; Search time 2045 Seconds (without alignments) 7879.642 Million cell updates/sec
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                                                                                                                                                                                                                                          CAAATCGTCACCGACAATTC..........TAACTTTGGATAAAACAAT 663
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           GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                     22781392 segs, 12152238056 residues
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                                                                                    nucleic search, using sw model
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CD458837
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AQ447125
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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RESULT 2
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Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science, plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
CD458837 921 bp mRNA linear EST 03-JUN-2003 Fg08_04b10_A Fg08_AAFC_ECORC_Fusarium_graminearum_complex_substrate Gibberella zeae cDNA clone Fg08_04b10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are presented as their reverse complement and have been trimmed to
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                                                                                                                                                                                                                                                                                                                                                           CTGTTCGACGCAACAAGCGATCCAGCGGATCCGTCAACACCGGTGCTCACTTCCAGGCCT
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/note="Vector: pMBIBS-FLJ; Site 1: XhOI; Site 2: XhOI; The
/note="Vector: pMBIBS-FLJ; Site 1: XhOI; Site 2: XhOI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
material from both time points was combined prior to RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into different DraIII sites of the
pMBIBS-FLJ vector (5-prime DraIII site is CACTGTGTG,
3-prime DraIII site is CACCATGTG). XhOI excises the cDNA
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/clone="ETH1_48_B06_A002"
/lab_host="DH10B-T1_phage_resistant_B._coli"
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Pred. No. 2.7e-09;
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1 (bases 1 to 921)
Watson, R.J., Heys, R., Chapado, J., Lacroix, C., Ouellet, T.,
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CD458837.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (613) 759-1655
Fax: (613) 759-1701
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Hypocreomycetidae; Hypocreales; Nectriaceae; C
                                                                                                                                                                                                                    CCATCCGCCGCAACAAGCGTACCAGCGGCTCCGTCAACATGCAGAACCACTTCAATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                       GCAGCCAGGCTCAGCACCGAGGTACCGTCTACACCGACGGTGACACCTACGATCTCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGA----GCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCAC
                             ACCAGAGCAGTGGCTCATCTTCTATCTATGTCCAGAC
                                                                      ATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATAC 593
                                                                                                                          GGAGATCTGCTGGCATGAACCTCGGAAACCACTACTACCAGATTCTGGCCACTGAGGGTT
                                                                                                                                                                                                                                                              GTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGT
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                                                                                                                                                                   GGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XhoI, Fusarium graminearum grown on a complex plant substrate-- wheat leaves treated to remove most of the low molecular weight, water-soluble components."

254 c 232 g 232 t
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/clone="F908_04b10"
/tissue_type="Mycelium"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli_DH10B"
/clone_1b="F908_AAFC_ECORC_Fusarium_graminearum_complex_s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Gibberella
/mol_type="mRNA"
/strain="DAOM 180378"
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let,T., Robert,L.S., Singh,J.A., Sprott,D.
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Clemson University Genomics Institute
Clemson University
Clemson University
Il00 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
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Best Local Similarity 54.6%; Pred. No. 2.6e-08;
Matches 209; Conservative 0; Mismatches 168;
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/mol_type="genomic DNA"
/strain="70-15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 263.
Location/Qualifiers
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GSS.
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AQ447125/c
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/tissue_type="Protoplasts"
/lab host="E. coli DH108"
//lone lib="Cutor liber Black Library"
/clone lib="Cutor Rice Black EAC Library"
/clone lib="Cutor Rice Black EAC Library"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request." I others
                                                                   mgxb0006C21r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0006C21r, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 603)
1. (Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                  Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota, Fungi; Ascomycota, Perizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jozdan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Class: BAC ends
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Location/Qualifiers
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/db_xref="North Hands"
/db_xref="Taxon:148305"
/clone="mgxb0005C20f"
/tiseuc_type="Protoplasts"
/lab host=="E. Coli DH108"
/lab host=="E. Coli DH108"
/clone_lib="Cud1 Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
/note="Vector: pBACWICH; Site 1: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 91c clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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mgxb0005C20f CUGI Rice Blast BAC Library Magnaporthe grisea genomic
AQ447128
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204 AACCAGCCTCCATCGACGCACCAAGACCTTTCAGCAGTTCTGGTCGGTGCGCGCCAAC 145
                                                                              510
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Yu.Y., Zhu.H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                              144 AAGCGCCCAGCGCACCGTCACCTTTGCCAACCACGTCAACGCCTGGCGCAACGCCGGC
                                                                           451 AAACGCACGAGGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTTAGGG
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Magnaporthe grisea
Magnaporthe grisea
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Clemson University Genomics Institute
Clemson University
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Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,ps,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
/tissue_type="Protoplasts"
/lab host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/clone_tib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH, Site 1: HindIII, Site_2: HindIII;
/note="Vector: pBACWICH, Site_1: HindIII, Site_2: HindIII;
/note="Vector: pBACWICH
                                                                                                                                                                                                                                                                                                              /organism="Magnaporthe
/mol_type="genomic DNA'
/strain="70-15"
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Query Match
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AGCAGCGGCTCCGCCA
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                                                                                                                                                                                                                                                                                                                                                                                             GCCACCAACCGCGGGTCCTTCACCTCGGACGGCAGCACCTACGACATCCTGGTCAGCACC
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                                           AGTAGCGGAAGTGCTA
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Pred. No. 2.6e-08;
0; Mismatches 189
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Clemson University
100 Jordan Hall, Clemson U
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu Magnaporthe grisea (anamorph: Pyricularia grisea) Magnaporthe grisea Eukaryota; Fungi; Ascomycota; Pezizomycotina; Soi Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.? A BAC End Sequencing Framework to Sequence the Ma AQ160254 750 bp DNA linear (mgxb0003119r CUGI Rice Blast BAC Library Magnaporthe Seq primer: GGAAACAGCTATGACCATGClass: BAC ends Clemson University Genomics Institute Unpublished Contact: De Genome AQ160254.1 High quality sequence Sordariomycetes incertae sedis; clone mgxb0003L19r, genomic survey sequence. (bases 1 to 750) Dean RA GI:3557243 stop: 344 Universiy, Magnaporthaceae; Clemson, the Magnaporthe grisea ၁၁ Sordariomycetes; Magnaporthe. Kingsbury, R., GSS 09-S e grisea 09-SEP-1998 isea genomic

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/tissue type="Protoplasts"
/tissue type="Protoplasts"
/lab_host="E. coli DH10B"
/clon=lib="CGCI Rice Blate BAC Library"
/clon=lib="CGCI Rice Blate BAC Library"
/note="Vector: pBAGWICH; Site 1: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request." I others
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                          Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 GCCGGCCTCAACCTCGCAACCAGTGGAACTACCAGATCCTGGCCGTCGAGGCTTACCAC 86
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                                                                                                                                                 Contact: Dean RA
Clemson University Genomics Institute
Clemson University
University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 4293
Fax: 864 656 4293
Fax: 864 656 4293
Fax: 864 primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 49
High quality sequence stop: 468.
Location/Qualifiers
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Pred. No. 3.6e-08;
0; Mismatches 189;
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/mol_type="genomic DNA"
/strain="70-15"
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/clone="mgxb0021M08r"
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          (bases 1 to 786)
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/tissue type="Troplasts"
/lab host="E. coli DH108"
/clon=lib="Cud1 Rice Blast BAC Library"
/note="Vector: pBAGWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request." 2 others
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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Pred. No. 2.6e-08;
0; Mismatches 189;
                                                         grisea"
                                                    /organism="Magnaporthe | /mol_type="genomic DNA" | strain="70-15"
                                                                                                                            _xref="taxon:148305"
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Location/Qualifiers
1. .750
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                                                                                                                                                                                                                                                                                               Query Match 12.3%;
Best Local Similarity : 52.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 864 656 5737
Pax: 864 656 4293
Email: rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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AQ399120.1 GI:4370147
GSS
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CTGATCGAGTACTACGTGGTGGAGAGCTTTGGCAGCTACAACCCGTCGTCGGGCGCCACC 266
                                                                                                                             GCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGTTGGACTGTTGACCCT
                                                                                                                                                                                  AAGAAAAAAAGAGAGACTAACATCAACAACAACAAAAAACAGCCGCGTCATCAACTACTCG 386
                                                                                                                                                                                                                              AAAAAATTCAATGAAACACAAACACCAACAAGTTGGTAACATGTCCATAAACTACGGA 213
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on Tordan Hall, Clemson Universiy, Clemson,
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                                         CITGICGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACCA---GGAGCAACG 330
                                                                                       GGCAGCTACAGCCCACAGGGCAACTCATACCTGGCCGTCTACGGCTGGACGCGCAACCCG
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Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Ilips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                           104
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Location/Qualifiers
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="CUGI Rice Blast BAC Library"
/clone lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="mgxb0001B24f"
/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
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Pred. No. 3.9e-08;
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ACCESSION
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AQ396475
AQ396475.1 GI:4367502
GSS
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Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGACTCACTATAGGG
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                        99
            /lab host="E. Coli DHIOB"
//LIONE 11b="CUGI Rice Blast BAC Library"
//Clone 11b="CUGI Rice Blast BAC Library Blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
99 a 135 c 187 g 137 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA'
/strain="70-15"
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/clone="mgxb0010M14f"
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Query Match 11.6%; Best Local Similarity 53.7%; Matches 204; Conservative

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Score 76.6; DB 28; Pred. No. 4.7e-07; 0; Mismatches 170;

Indels Length 561;

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numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request."
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Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 GACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTGGCGTCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 TGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTG
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                             11.3%; Score 74.6; DB 28; Length 753; 55.1%; Pred. No. 1.4e-06; ive 0; Mismatches 134; Indels 3
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson,
Tel: 864 556 5737
Email: rdean@clemson.edu
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/organia="Magnaporthe grisea"
/mol type="genomic DNA"
/strain="70-15"
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Class: BAC enda
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/lab host="E. coll DH108"
/clon=lib="CGIZ Rice Blast BAC Library"
/note="Vector: DBACWICH; Site 1: HindIII; Site 2: HindIII;
/note=vector: DBACWICH; Site 1: HindIII; Site 2: HindIII;
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
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                                                                               --CATCAACTACTCGGGCAGCTACAGCCCCAGGGCAACTCATACCTGGCCGTCTACGGC 379
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Y.Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips K., Sasinowski, M. Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 TCGTCGGGCGCCACCAACCGCGGGTCCTTCACCTCGGACGCCAGCAACTACGACATCCTG
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                                         TTATTCCGTAAAAGGTAAAAATTCAATGAAACACAAAACACACCAACAAGTTGGTAACATG
                                                                                                                                                                                 TCCATAAACTACGGAGCCAACTTCCAACCAAATGGTAATGCGTATTTATGCGTCTATGGT
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Magnaporthe grisea
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; Sordariomycetes; Sordariomycetes; Magnaporthaceae; Magnaporthe.
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Contact: Dean RA
Contact: Dean RA
Clemeon University Genomics Institute
Clemeon University
100 Jordan Hall, Clemeon University, Clemeon, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemeon.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 401.
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/mol_type="genomic DNA"
/strain="70-15"
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/tissue_type="Protoplasts" /lab_host="E._coli_DH10B"

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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Vernalized crown cDNA library
Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service,
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ165950 520 bp mRNA linear EST 25-APR-2002 WHE0821-0824 F22 F22ZT Wheat vernalized crown cDNA library Triticum aestivum cDNA clone WHE0821-0824 F22 F22, mRNA sequence
                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
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//clone lib="CUGI Rice Blast BAC Library"
//clone lib="CUGI Rice Blast BAC Library"
//note="Wector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
/note="Wector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
/note="Wector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
/note="Wector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
/note= blast is one of the most devestating fungal between for studying numerous aspects of the fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
61 a 104 c 161 g 91 t 1 others
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595818
Email: oandersn@pw.usda.gov
This EST was generated by sequencing from the 3' end of the clone.
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20.
Seq primer: T7 primer.
                                                                                                                                                                                                                                                                   BQ471960 561
HV04A02r HV Hordeum vulgare
                                                                                                                                                                                                                                              5-PRIME,
                                                                                                                                                                                   BQ471960.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGGGTTACCAGTCTTCTGGCAGCTCGGACATCTATGTGCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAGGCTATCAAAGTAGCGGAAGTGCTAATGTATATAGCAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTACTGGTCTGTCCGCACGCAGAAGCGCGTCGGAGGCAGCGTCAACATGCAAAACCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCTACGAGACTCTTAGAGTCAATCAACCCTCCATTAAGGGGGATTGCCACATTTAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAACCCCAGCAGCGGATCCCAGCGCAAGGGCAGCTTCACGACTGACGGCGGTACCTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGTCC---ACCAGGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTATGGTTGGACTGTTGACCCTCTTGTCGAATATTATATTGTCGACAGTTGGGGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACGCCTGGGCTCGTTACGGCATGAACTTGGGCCCAGCACTACTACCAGATTGTCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGAGCGTGGGAAAACTTAGGGATGAATATGGGGAAAATGTATGAAGTCGCGCTTACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATATTGGAGTGTTCGAAGATCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTTCCACCTCCACCCGTACCAACCAGCCCTCCATCGATGGAACAAGGACCTTTCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACGGTTGGACCCGCAACCCGCTTGTGGAGTACTACGTGATCGAGTCTTACGGCACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Wheat vernalized crown cDNA library",
/note="Vector: Lambda Uni-Zap XR, excised phagemid;
Site_1: EcoRI, Site_2: XhoI, Seeds were germinated and
grown at 4 C for 5 weeks. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                              m.R.N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0821-0824 F22_F22"
/tissue_type="Crown tissue of seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dev_stage="Five-week old seedling"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                   GI:21279742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5%;
                                                                                                                                                                                                                                        sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69.8; DB 1: Pred. No. 1.6e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 162;
                                                                                                                                                                                                                                                                          empap.
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                                                                                                                                                                                                                                                                          vulgare
                                                                                                                                                                                                                                                                          cDNA clone HV04A02
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Gaps

488

281

221

428 341

401

461

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396

BASE COUNT

61

Query Match Best Local Similarity

11.2%;

Score 74.4; Pred. No. 1.

Mismatches 172; .4e-06; DB 28;

Matches 203;

Conservative

용

JOURNAL COMMENT

TITLE

REFERENCE

Triticeae; Tritic (bases 1 to 520)

EST 30-MAY-2002

AUTHORS

RESULT 12 BQ165950/c

DEFINITION

밁 ş 밁 ঠ

96

500 156 440 216 380 276 322 336 263

밁 5

36

ACCACAGCAGCGGCTCCGCCA 16

557

ATCAMAGTAGCGGAAGTGCTA 577

ACCESSION VERSION

BQ165950 BQ165950.1 GI:20308866

KEYWORDS

EST

SOURCE ORGANISM

Triticum aestivum

Triticum aestivum (bread wheat)

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Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.B., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O., Eastman, A. and Pratt, L.H.
An EST datebase from Sorghum: 1-aminocyclopropane-1-carboxylic acid (ACC)-treated seedlings
                                                                                                                                                                                                                                                                                                                                                                                           Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University plant material and RNA prepared at Texas A & M University, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude exclude polyA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 CAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGATCGAAA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 cGATCCAGCGGATCCGTCAACACCGGTGCTCACTTCCAGGCCTGGAAAATGTCGGCCTC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 AAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACGAGACTCTTAGAGTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 GCCCCCTCCATTGAGGGTAACAAGCCCTTTCAGCAGTTTTGGTCTGTTCGACGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 CGCACGAGTGGCACGATTTCTGTCAGCAACCACTTTAGAGCGTGGGAAAACTTAGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 ACCCTTGGTAACCACAACTATCAGATCCTTGCTGTTGAGGGCTACTACAGCTCTGGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AAGGGTGAGGTCACTGTTGACGGATCTGTTTACGACATTTACGTCAGCACCCGTCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 AATATGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGCGGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tal: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 63.2; DB 14; Length 473; 53.7%; Pred. No. 0.0005; ive 0; Mismatches 113; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Sorghum bicolor"
                                                                                                                                                                                              Other ESTs: ETH1 48 B06.g1 A002 Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                         Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 53.7
Matches 131; Conservative
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ORIGIN
       REFERENCE
AUTHORS
                                                                                                                                                                             JOURNAL
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                                                                                                                            TITLE
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/note="Vector: pBluescript SK+; Site_l: EcoRI (5'-end of CDNA); Rocts were grown for CDNA); Site_l: Xho! (3'-end of CDNA); Rocts were grown for two days on filter paper at room temperature. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRiadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, Pst!).

NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable. Average
1 (bases 1 to 561)
Zhang, H., Potokina, B., Michalek, W., Weschke, W., Stein, N. and Graner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #473 bp mRNA linear EST 04-JUN-2003 ETH1_48_B06.bl A002 Ethylene-treated seedlings Sorghum bicolor CDNA Clone ETH1_48_B06_A002 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 cearcaactacececarcrirceaccreaegeraacerracerreceiriacearra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 GGACTGTTGACCCTCTTGTCGAATATTATTGTCGACAGTTGGGGGCAACTGGCGTCCAC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 GGACCCGCAACCCGCTTGTGGAGTACTACGTGATCGAGTCTTACGGCACCTACAACCCCA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 CA---GGAGCAACGCCTAAGGGGACCATCACTGTTGATGGAGGAACATATGATATCTACG 376
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435
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                                                               Marley ESTs from germinating seeds
Unpublished
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3.06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5525
Email: stein@ipk-gatersleben.de
Insert Length: 561 Std Brror: 0.00
Plate: 4 row: A. column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 10.0%; Score 66.2; DB 13; Length 561; al Similarity 57.7%; Pred. No. 0.00011; 138; Conservative 0; Mismatches 98; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:112509"
/clone="HV04A02"
/clssue_type="germinating seeds"
/dev stage="germinating seeds (48-96 h)"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insert size is 1 kb"
                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 g
                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD464005.1 GI:31385273
                                                                                                                                                                                                                                                                                                                                             Seg primer: M13rev.
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Matches 13
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ORGANISM
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JOURNAL
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VERSION
KEYWORDS
REFERENCE
AUTHORS
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AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                271 CCTCTTGTCGAATATTATTGTCGACAGTTGGGGCAACTGGCGTCC---ACCAGGAGCA 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: stein@ipk-gatersleben.de
Insert Length: 483 Std Error:
Plate: 4 row: A column: 2
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Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensetr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Stein Nils
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TCGAAACGCACGAGTGGCACGATTTCTGTCAGCAACCACCTTTAGAGCGTGGGAAAACTTA 507
                                                                                                                                                                                  GTCAATCAACCCTCCATTAAGGGGATTGCCACATTTAAACAATATTGGAGTGTTCGAAGA 447
                                                                                                                                                                                                                                                         CAGCGCAAGGGCAGCTTCACGACTGACGGCGGTACCTACGACGTTTCCACCTCCACCCGT
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ilarity 51.2%;
Conservative
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/clone lib="lib"

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/dev_stage="germinating seeds (48-96 h)"
/lab_host="XL10-Gold"
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/cultivar="barke"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="HV04A02"
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Pred. No. 0.0021;
0; Mismatches 156;
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GGCAGCTCGGACATCTATGTGCAGAC 158
                                      GGAAGTGCTAATGTATATAGCAATAC 593
                                                                            GGCATGAACTTGGGCCAGCACTACTACCAGATTGTCGCCACTGAGGGTTACCAGTCTTCT 184
                                                                                                                   GGGATGAATATGGGGGAAAATGTATGAAGTCGCGCTTACTGTAGAAGGCTATCAAAGTAGC 567
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Search completed: October 20, 2003, 12:03:43 Job time: 2051 secs